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705					710					715					720
Gln	Arg	Leu	Ile	Ala	Pro	Gln	Thr	Leu	Asn	Leu	Thr	Ala	Val	Asn	Glu
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Ala	Val	Leu	Ile	Glu	Asn	Leu	Glu	Ile	Phe	Arg	Lys	Asn	Gly	Phe	Asp
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		755					760					765			
Ser	Leu	Pro	Thr	Ser	Lys	Asn	Trp	Thr	Phe	Gly	Pro	Gln	Asp	Val	Asp
	770					775					780				
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785					790					795					800
Ser	Arg	Val	Lys	Gln	Met	Phe	Ala	Ser	Arg	Ala	Cys	Arg	Lys	Ser	Val
			805				810							815	
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Asn	Leu	Thr	Thr	Tyr	Gly	Phe	Arg	Gly	Glu	Ala	Leu	Ser	Ser	Leu	Cys
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Glu	Arg	Asp	Leu	Phe	Ile	Val	Asp	Gln	His	Ala	Ala	Asp	Glu	Lys	Phe
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2161   AGA AAA AAC GAA ATG CAG AAG ATA GTA GAA CAC TTG GCA GAT CTC GAA TCT CCT TGG AAT
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 121 GTC AAG GAG CTT GTC GAG AAT AGT CTC GAC GCC GGC GCC ACC AGT ATA GAG ATT AAC CTC
 R D Y G E D Y F Q V I D N G C G I S P T
 181 CGA GAC TAC GGC GAA GAC TAT TTT CAG GTC ATT GAC AAT GGT TGT GGC ATT TCC CCA ACC
 N F K V C V Q I L R R T F D V L A L K H
 241 AAT TTC AAG GTT TGT GTC CAA ATT CTC CGA AGA ACT TTT GAT GTT CTT GCA CTT AAG CAT
 H T S K L E D F T D L L N L T T Y G F R
 301 CAT ACT TCT AAA TTA GAG GAT TTC ACA GAT CTT TTG AAT TTG ACT ACT TAT GGT TTT AGA
 G E A L S S L C A L G N L T V E T R T K
 361 GGA GAA GCC TTG AGC TCT CTC TGT GCA TTG GGA AAT CTC ACT GTG GAA ACA AGA ACA AAG
 N E P V A T L *
 421 AAT GAG CCA GTT GCT ACG CTC ...

Sequence ID 6. *Arabidopsis thaliana* PMS134 homologue cDNA and amino acid sequences.

1 70

humPMS2 (1) ATGGAGCSAGCTGAGAGCTCGAGACAGAACTGCTAAGGC-----ATCAAACCTATGATCGGAAGT

AtPMS2 (1) ATGCAAGCAGATTCTTCTCCGTC--CGAGACTACTAGCTTCCTTTGATAAGACCTATAACAGAAACG

Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA

71 140

humPMS2 (65) CAGTCTCAGATTTGCTGCTGGG--AGGTGGTACTGAGTCTAAGCACTGCGGTAAGGAGT--AGTAGAAG

AtPMS2 (71) TAAATTCAGAAATCTCTTCGGTCAAGTCACTAGACCTCTCTTGGGCGTCAAGGAGCTTTTCAGAA

Consensus (71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA

141 210

humPMS2 (135) CAGTCTCGATGCTGGTGGCAGTATATTATATCTAAAGCTTAAGGACTATGGATGGATCTATTGAAGTT

AtPMS2 (141) TAGTCTCGACCCGGCCGCCACCTGATAGAGATTAACTCCGAGACTACGGCAGAGACTATTTTCAGCTC

Consensus (141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT

211 280

humPMS2 (205) TCAGACAATGGATGTGGGT-----AGAAGAAG-----AAAACCTCGAAG-----G

AtPMS2 (211) ATTGACAATGGTTGTGGCATTTCCCAACCAATTCAGGTTTGTGTCCAAATTCCTCGAAGAACTTTTG

Consensus (211) GACAATGG TGTGG T A AAG AA CT CGAAG G

281 350

humPMS2 (246) CTAACT---CTGAACATCAACATCTAAGATCTAAGAGTTTGGCGACCTAACTCAGCTGGA--ACT

AtPMS2 (281) ATGTTCTTGCACTTAAGCATCATCTTCTAAATTAGCGATTTCAAGATCTTT--CAAT--TGACTACT

Consensus (281) T CT CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT

351 420

humPMS2 (311) TTGGCTTTCCGGGSAAGCTCTCAGCTCACTTTGTGCACTGACCGATGTCACCAITTTCTCTC--CCAC

AtPMS2 (350) ATGGTTTTCAGGAGAAAGCTTCAGCTCTCTCTGTGCACTGCGAAATCTCACTGTGGAA--AAAGAA

Consensus (351) TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A

421 490

humPMS2 (379) GCATCGCCGAGGTGTGAAGTCTGATGATTTTGATCAAAATGGGAAATTA--TCCAGAA--CCCCCTAC

AtPMS2 (420) GAATGAGCA--GTTGCTACGTTCTGCTGATGATCTTCTGCTTGTGCTTACCTGTA--GAAGACTG

Consensus (421) G AT GC A GTTG AC C TGA GTTGTATCA TGG TTA T C GAAA

491 560

humPMS2 (448) CCGCCGCCGAGGCAACCACTGACGCTGCAACAGTTATTTCGACCTACCTGTGGCCATAGGAAT

AtPMS2 (488) CTG--GCCAAATTTGTAACCACTCTCACTGTAGCAAGTTGTTCTCTTATTACCTGTACCAAGCAAGAG

Consensus (491) C C GCC A GG ACCAC GTCA GT G AGTT TT TC A TACCTGT CG AA GA T

561 630

humPMS2 (518) TTCAAAGGAATATTAAGAAGGAGTATGCCAAATGGTCCAGGCTTACATGTCATACTGTATCATTTAGC

AtPMS2 (557) TTAAAGCGAATATACGAAAGAAATATGGAAGGCTTGTATCTTTATTGAACGCATATGCGCTATTGCGAA

Consensus (561) TT A GGAATAT AA GA TATG AA T GT T TT A GCATA T ATT C

631 700

humPMS2 (588) AGGCATCCGTCTAAGTTGGACCTCTCAGCTTGCACAAAGAAACGACGCTGTGGTATGCACAGGTCGA

AtPMS2 (627) AGGAGTCCGCTTGTCTGCTCTCACCAGCTGGGAA--AACCGAAGTCTGTGTG-----CTCA

Consensus (631) AGG T CG T TGC C AA G TGG AA AA C A AG CTGT GT G GA

701 770

humPMS2 (658) AGCCCAAGCATAAAGGAATATCGGCTCTGTGTTTGGCAGAACAGTTGCAAGCCTCATTCTTTTG

AtPMS2 (686) A---CA--CAAA--GGG-----G--GG-----G

Consensus (701) A CA CA AA GG A G G G

771 840

humPMS2 (728) TTCAGCTGCCCTAGTGACTCCGCTGTGTGAAGAGTACGGTTTGAGCTGTTCCGATGCTCTGCATATCT

AtPMS2 (702) TTCA-----CT--TAAAG--TAA--ATCTAAGCAATTT-----TCGCATTAGTA

Consensus (771) TTCA C TA GA T A A AC GTTT TC GCAT A

841 910

humPMS2 (798) TTTTACATCTCAGGTTTCATTTCACAAATGCAACCATGGAGTTGGAAGAGTTCAACAGACAGACAGTT

AtPMS2 (743) CTTTACAAGT-----TACA--GCCTGGTACTGGACGCAATTAGCAGATCGACAGTA

Consensus (841) TTTACA TC T CA GC TGG TGA G A TT A CAGA GACAGT T

911 980

humPMS2 (868) TTCTTTTATCAACCGCGGCTTGTGACCCAGCAAAGTCTGCAAGCTCTGGAATGAGCTTACCAATG

AtPMS2 (796) TTCTTTTATAATGCTCGGCTGTAGATATGCCAAAGTCAAGAGTTGGTGAATGAGTATAT--AAGAG

Consensus (911) TTCTTTTAT AA G CGGCT GA CAAA GTC GCA T GTGAATGAG T TA A A T

981 1050

humPMS2 (938) AATA--TCGACACCATATCCATTTGTTGTTCTTAACATTTCTGTGATTCAGATGCGGTGATATCAATG

AtPMS2 (865) ACAAAGTCTCGGAATATCCAGTACCATCTCTGCATTTATGTGCTTGGTGGCATGCTATTTGAATG

Consensus (981) A AA T C A TATCCA TT TTCT A TT TGT T G A TGAT T AATG

1051 1120

humPMS2 (1007) TTACTCCAGATAAAAGGCAATTTTGTCTCAAGAGGAAAGCTTTTGTGGCASTTTTAAAGACCTCTTT

AtPMS2 (935) TCAGCCCGATAAAAGAAAGGCTTTCTTTCTGACGAGA--CTTCGTTATCGSTT-----CTTT

Consensus (1051) T AC CC GATAAAAG A T TT T GA GA A CTT GTTT C GTT CTTT

1121 1190

humPMS2 (1077) GATAGGAATGTTTGAATAGTATGTCTACAGAGCTAAATGTCAGTCAGCAGCCACTGCTGGAATGTTGAAGT

AtPMS2 (993) GAG--GGAAGGTCTGA-----A--CGAGATATATCC--H-----CCAGTAATGCGCTTATA---

Consensus (1121) GA GGAA GT TGA A C AG TA AT C T CCA T TG T TT A

1191 1260

humPMS2 (1147) AACTTAATAAAATTCATTCACCGGATTTCGAAAGGCCATGGTAGAAAGCAGGATCAATCCCGTTCA

AtPMS2 (1040) ----TTGTTAATAGTTTCAGGAGATTTCGGAGCAACG-----AGATAAG--GCTGGGTTTGTGCT

Consensus (1191) T T AA A G G G G ATT GGA A CC AGA AAG G T A C TC T

1261 1330

humPMS2 (1217) TAAGGACTGCGAAGAAATAAAAGACGTGTCATTTTCAGACTGCGAGAGCCTTTTCTCTCTCAGCAC

AtPMS2 (1097) TTC-----AGAAGAAATCAAA--TCTTTTGTTCAGAA--GGATAG-----TTCTGGATGTCAGTT

Consensus (1261) T AGAAGAAA AAA TC TT CAGA G GA AG TTCT GTCA 1400

1331

humPMS2 (1287) AACAGAGAACAGCCTCACAGCCCAAGAGCTCCAGACCAAGAGGAGCCCTCTAGGACAGAAAAGGGCT

AtPMS2 (1148) CTAA--AACAGACT--AGGGGAAGCTATTGAGAGAGAAAATCCATCCTTAAGGAGGTTGAAATTCGA

Consensus (1331) A AACAG CT AG AA T AGAA AA A A CC T GGA AA G

1401 1470

humPMS2 (1357) ATGCTCTTCTGCACTTCAGCTGCCATCTCTGACAAAGGCGTCTGAGACCTCAGAAAACAGGCAGTGA

AtPMS2 (1212) TAATAGTTCCGCATGAGAGAAGTTTAAGTTTGAGATCAGGCAATG-TGCGACGA-AGAAAAGGGGAAG---

Consensus (1401) GT C A AG T T T GA AAGGC T TG GAC AGAAAAG GG AG

1471 1540

humPMS2 (1427) GTTCAGTTCGACCCAGTGAACCTACGACAGAGCGAGGTGAGAGGAGTTCGGGGCAGGCAGCAC

AtPMS2 (1277) GTTCT--TGT--CAGT--CCAT--SATGTAAATCCCTTGAACAG-AGACCTAGCAAAAGTTTGC

Consensus (1471) GTTC T A CAGT CC GA A C A T GA AAG AC C GCA G C

1541 1610

humPMS2 (1497) TTCCGTGGATCTTGAGGGGTTTCAGCATCCGAGACACGGGAGTCACTGCAAGCGGAGTATGCGGCGAGC

AtPMS2 (1334) CTCAGTTAAATGTGACTG-----AGA-----AAGTTACTGATSCA--AGTA-----AAG

Consensus (1541) TC GT A T TGA G AGA AGT ACTG GCA AGTA A

1611 1680

humPMS2 (1567) TCCAGGGGACAGGGGCTCGCAGGAAACATGTGAGCTCTCAGGAGAAAGCGCTGAAACTGACCACTCTT

AtPMS2 (1376) ACTTGAG--CAGCCGCTCT--A-GCTTGCCTCAGTCA-----ACTT--TGAATCTCTTT

Consensus (1611) C AG CAG GCTC A T TG C TCA CT TGA ACT TT

1681 1750

humPMS2 (1637) TTTCAGATCTGACTGCCATTCAACCCAGCAAGATTCGGATGTAAATTTTCAGATTTTGCCTCAGCCACAG

AtPMS2 (1423) GTTACCATGGG-----AAA--AAGAAAC--ATGAAAC-----ATAAGC--AC

Consensus (1681) TT ATG G AAA AAGA A C ATG AAA C T AGC AC

1751 1820

humPMS2 (1707) TAACTCTGCAACCCCAACACAAAGCGTTTAAAGAAAGAGAAATTCCTTCCAGTTCTGACATTTGTCAA

AtPMS2 (1461) CATCTCTCTG--AAACACCT--CTCCTCAAAACCA--AACTCT--AGTTAT--CGTGTGGAGA

Consensus (1751) A CTC C AAACAC GT T A AAA A AA TTCT AGTT T C T TG A

1821 1890

humPMS2 (1777) AAGTTAGTAAATACTCAGGACATGTGAGCCTCTCAGGTTGATGTAGCTGTGAAAAATTAATACAAAGTTG

AtPMS2 (1517) AA--AGCAAA--TTGAAGTTCTGTC-----CTTGGTTCT--AGGTC--CTCGT--GGAAGGCG

Consensus (1821) AA AG AAAT AG C TG CT AG TT A AG TGT T T G AAG G

1891 1960

humPMS2 (1847) TGCCTCTGACTTCTCTATGAGTCTCTAGCTAAACAAATAAAGCAGTTACATCATGAGACAGCAAG

AtPMS2 (1568) ATGAAGTTG--TGATATG--G--TCATCTCAAA--GAGATTTGACACCAAGG--AAAG

Consensus (1891) C CT GA T TATG G T A CT AA G G AG TA CA AAGC AAAG

1961 2030

humPMS2 (1917) TGAAGGGGAACAGAATTACAGGAAGTTAGCGCAAAATTTGCTCTGGAAGAAATCAAGCAAGCCGAAAT

AtPMS2 (1620) AGATTTCTGAAGT-----AGGCAATC--G--BATTTCCTCTGGAAAC--CAAGCTCATATCTT

Consensus (1961) GA GAAC AGG A T G GATTT TCCTGGA A CAAGC G A G T

2031 2100

humPMS2 (1987) GAACTAAGAAAGAGATTAAGTAAGAGATGTTTCAGAAATGGAATCAATGCTCACTTTAACTGGGAT

AtPMS2 (1672) GAA--AGCACTGAGAGA--ATA--G-----TCGGCAATTCATCTTGGCT

Consensus (2031) GAA AGA A GAGA A GTA C T GG CA TT AA CT GG T

2101 2170

humPMS2 (2057) TTATAATAACCAAACTGAATGAGGATATCTTCATAGTGGACAGCATGCGACGAGAGAACTATAACTTT

AtPMS2 (1712) TCATCATTCGAAATTTGAGGAGATCTGTTTCATTTGGATCAGCATGCGAGTGAATGAGAAATTCACCTT

Consensus (2101) T AT AT C AAA TG A GAT T TTCAT GTGA CAGCATGC C GA GAGAA T AACTT

2171 2240

humPMS2 (2127) CGAG-ATGCTGCAGCAGCAACCGTGTCTCGGGGCGAGGCTCATAGCA-CCTCAGACTCTCAACTTAA

AtPMS2 (1782) CGAACATTTACCAAGGTCA-ACTGTCTGAGCCAGCA-ACCCTTCTCCAGCTTTGAAGTGGAGCTCT

Consensus (2171) CGA AT GCA CA AC GT CT A GCA A CT A CA CCT GA T A T

2241 2310

humPMS2 (2195) CTGCTGTAAATCAAGCTGTTCTGATAGAAATCTGGGAATATTTAGAAACAATGGCTTTGATTTCTTTAT

AtPMS2 (1850) CTCGCAAGAGAGAAATTAAGTCTGTTTATGACATGCTTATTAACAGGGAATGGCTTTCTCTAGAGGA

Consensus (2241) CT C G A GAAG T TG TA A TGGA AT T AG A AATGGCTTT T T G

2311 2380

humPMS2 (2265) CGATGAAATGCTCCAGTCACTGAAAGGGCT--AAACTGATTTCTTGGCACTAGTAAAACTGGACCT

AtPMS2 (1920) GAATCAAGTGCTCC--TCCCGAAACACTTTAGCTACAGAGCGATTCCTTATAGCAAGATATCACCT

Consensus (2311) AT AA TGCTCC TC C GAAA CT A ACT CC T CC TAG AA AA ACCT

2381 2450

humPMS2 (2333) TCGGACCCAGGACCTCGATGAAGTGTCTTCATGCGAGCGAAGCGGCTGGGG-----TCATGTGCCCG

AtPMS2 (1988) TTGGAGTCCAGATCTTAAGACCTGATCTCACTCTAGSAGATACCATGGGCAATGTTCCGTTGCTAG

Consensus (2381) T GGA C A GA T A GA CTGATCT A CT G GA A CC TGGGG TC TGC G

2451 2520

humPMS2 (2398) -----CCCTCCGAGTCAAGCAGATGTTTGGCTCCAGAGC

AtPMS2 (2058) TAGCTACAAAACAGCAAAACAGATTGATTTGTCATCAGAGTCCGTGCAATGCTAGCATCCCGAGCA

Consensus (2451) CC TC CGAGTC ATG T GC TCC GAGC

2521 2590

humPMS2 (2434) TCCCGGAAGTCTGCTGATGATTTGAGCTCTCTTAAACCAAGCCAGATGACAAACTGATCACCAGATGG

AtPMS2 (2128) TCGACATCATCTGTGATGATCGAGATCCACTCTGAGAAAAACGAATGACAGAGATAGTAGAACACTTGG

Consensus (2521) TGC G TC GTGATGAT GG T C CT A A AA CGA ATG AGAA T T CAC TGG

2591 2660

humPMS2 (2504) GGAGAGTGGACCAACCGCTGGAACTGTCCCAATGGAAGCCCAACATGACACATCCCAAGCTGGGTGT

AtPMS2 (2198) CAGATCTCAATCTCGTTGGAAATGCGGACACGGACCAACAATGCTCATCTTCTGGAGTTGACAA-

Consensus (2591) GA T GA CC TGGAA TG CC CA GGA G CCAAC ATG G CA T G AC TG